



**Integrative Cancer Research Workspace
Proteomics Tools Special Interest Group
Mission Statement
DRAFT**

The opportunities /needs we address:

The Proteomics Tools SIG is focused on

- Tools and technologies which are necessary for cancer centers to store, annotate, and analyze the growing proteomics data sets
- Providing flexible tools for data and metadata storage, so that emerging technologies can be incorporated into developed systems
- Integrating proteomics data with other data through use of appropriate CDEs and architectures

What we are doing/will do to address these needs:

- The Proteomics Tools SIG will begin collaborations between developers and adopters to create laboratory information management systems (LIMS) linked to laboratory workflow to store data and metadata.
- The Proteomics Tools SIG will adapt existing analysis tools and integrate them through APIs to the developed databases in order to provide analysis capabilities linked to LIMS
- The Proteomics Tools SIG will work closely with Strategic Level and Cross Cutting working groups to incorporate common architectures, CDEs and structured vocabularies to assure proteomics tools are extendible across the caBIG community.
- The Proteomics Tools SIG will coordinate and collaborate with related proteomics standards efforts such as the EDRN and the emerging caProteo effort.

The principles/beliefs that guide our work:

- It is appreciated by the Proteomics Tools SIG that the field is rapidly evolving and that new technologies, data types, and analysis methods are likely to emerge in the next few years. As such a design principle for all systems will be flexibility to allow additions to existing systems without significant reengineering.
- Proteomics comprises only a part of the necessary data and methods for addressing the problems of understanding, treating, and controlling cancer, so integration of the tools created by this SIG with other SIGs is of paramount importance,